

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAQPaiHi: 995 aa

>SEQ ID NO:2

vs /tmp/fastaDAARPaiHi library

searching /tmp/fastaDAARPaiHi library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.050

The best scores are:

NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref (1008) 2671 opt

>>NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref NM_0 (1008 aa)

initn: 1414 initl: 972 opt: 2671

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

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      10      20      30      40      50
SEQ   MKILILGIFLFLCSPGWAIDRHCYIGIEESIWNYPSPGKNMLNEKPFSEDLE----FLQ
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 MKILILGIFLFLCSTPAWAKEKHYYIGIIEETTWDYA---SDHGEKKLISVDTEHSNIYLQ
      10      20      30      40      50

      60      70      80      90     100     110
SEQ   GGQARKSFVFKKALYFQYTDNTFQRIIEKPSWLGLGPMIKAETGDFIYVHVKNNASRAY
      ..:..:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 NGPDRIGRLYKKALYLQYTDFTRTTIEKPVWLGLGPIIKAETGDKVYVHLKNLASRPY
      60      70      80      90     100     110

      120     130     140     150     160     170
SEQ   SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPSPNDNSNCV
      ..:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV
      120     130     140     150     160     170

      180     190     200     210     220     230
SEQ   TRIYHSHIDTARDVASGLIGPILTCKRGTNLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN
      .....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 TRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDN
      180     190     200     210     220     230

      240     250     260     270     280     290
SEQ   IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGMGGVADIIH
      ....:..:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 IKTYCSEPEKVDKDNEFDQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFMGMGNEVDVH
      240     250     260     270     280     290

      300     310     320     330     340     350
SEQ   PVYLRGQTLISRNHRKDTIMLFSSLEDAFMVAKAPGVWMLGCQ----IHESMQAFFFKVS
      .....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 AAFHFGQALTKNKYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
      300     310     320     330     340     350
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	360	370	380	390	400	410
SEQ	NCQKPST	EAFVTGTHVIHY	YIAAKEILWNYAP	SGIDFFTKKNLTA	AGSKSQLFFERS	SPTR
NM_000	ECNKSSSKDNIR	GKHVRHYIIAAEE	IIWNYAPSGIDIF	TKENLTAPGSDS	AVFFEQGTTR	
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGTYKKLIYREY	TDASFQTQKAR--	EEHLGILGPVFKA	EVGQTIKITFYNN	ASLPLSI	
NM_000	IGGSYKKLVYREY	TDASFTRNKRERG	PEEEHLGILGPVI	WAEVGDTIRVTFH	NKGAYPLSI	
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGL	FYE---TPGG-ST	PPPSHHVSPGTT	FFVYTWEVPKDV	GPTSTDPNCL	
NM_000	EPIGVRFNKNNEG	TYSPNYPQSRSV	PPSASHVAPTET	FITYEWTVPKEV	GPTNADPVCL	
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFYYSVNGKKDIN	SGLLGPLLICRNG	SLGDDGKQKGV	DKEFYLLATIFD	ENESNLLDE	
NM_000	AKMYSAVDPTKDIF	TGLIGPMKICKK	GSLHANGRQKD	VDKEFYLFPTV	FDENESLLED	
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFITEPENID	KEDTDCQASNKM	YSINGYMGNLPL	GLDTCGLDNVL	WHVFSVGSVED	L
NM_000	NIRMFTTAPDQVD	KEDDFQESNMK	HSMNGFMYGNQ	PGLTMCKGDS	VVWYLF	SAGNEADV
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSL	GARDTIPMFYTS	QTLLMTPDSIG	TFDLVCMTIKHN	LGGMKHKYHV	
NM_000	HGIYFSGNTYLWR	GERRDANLFPQ	TSLTHMWPDT	EGTFNVECLTT	DHYTGGMKQKY	TV
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCGKPNPDQTQY	QEEKIIITIAAE	MEWDYSPSRKWE	NELHHLRRENQ	TSMYVDRSGL	L
NM_000	NQCRQSEDSTFY	LGERTYY-IAA	VEVWDYSPQRE	WEKELHHLQEQ	NVSNFLDKGE	FY
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQY	DDNTFTNQTRNE	GKHLDLGPLILL	NPGQIIQIIFKN	KAARPYSI	
NM_000	IGSKYKKVVYRQY	TDSTFRVPVERK	AEEEHLGILGP	QLHADVGDKVI	IFKNMATR	PYSI
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHGVKTNNSTV	VPTQPGEIQIYT	WQIPDRTGPTSL	DFECIPWFYYST	VSVAKDLHSG	LV
NM_000	HAHGVQTESSTV	PTPLPGETLTY	VWKIPERSGAG	TEDSACIPWAY	YSTVDQVKD	LYSGLI
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ   GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      :::  :::  :  :::  ..  .:  .....:
NM_000 GPLIVCRRPYLKVFNP RRKLEFALLFLVFDENESWYLD DNIKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ   SNQMHAINGRLFGNNQGITFHVGDVWNWYLIGIGNEADLHTVHFHGHHSFEYKHKYLI
      .....: .....: .....: .....: .....:
NM_000 SNKMHAINGRMFGNLQGLTMHVGDEVN WYLMGMGNEIDLHTVHFHGHHSFQYKHR
      960      970      980      990      1000

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995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA